Amendments to the Specification

Please replace the paragraph beginning at page 14, line 21, with the following amended paragraph.

The present invention further includes MscCa polypeptides having similarity with the amino acid sequence of SEQ ID NO:2. The similarity is referred to as structural similarity and is generally determined by aligning the residues of the two amino acid sequences (i.e., a candidate amino acid sequence and the amino acid sequence of SEQ ID NO:2) to optimize the number of identical amino acids along the lengths of their sequences; gaps in either or both sequences are permitted in making the alignment in order to optimize the number of identical amino acids, although the amino acids in each sequence must nonetheless remain in their proper order. A candidate amino acid sequence is the amino acid sequence being compared to an amino acid sequence present in SEQ ID NO:2. A candidate amino acid sequence can be isolated from an animal, preferably a human, or can be produced using recombinant techniques, or chemically or enzymatically synthesized. Preferably, two amino acid sequences are compared using the Blastp program of the BLAST 2 search algorithm, as described by Tatusova, et al. (FEMS Microbiol. Lett, 174:247-250 (1999)), and available ~~at http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html~~ through the World Wide Web at the internet site maintained by the National Center for Biotechnology Information, National Institutes of Health. Preferably, the default values for all BLAST 2 search parameters are used, including matrix = BLOSUM62; open gap penalty = 11, extension gap penalty = 1, gap x_dropoff = 50, expect = 10, wordsize = 3, and optionally, filter on. In the comparison of two amino acid sequences using the BLAST search algorithm, structural similarity is referred to as "identities." An MscCa polypeptide may include an amino acid sequence having a structural similarity with SEQ ID NO:2 of at least 90 %, for example at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or at least 100 % identity. An MscCa polypeptide having structural identity to SEQ ID NO:2 typically has the structural features common to the TRP family (Wes et al., Proc. Natl. Acad. Sci. USA, 92:9652-9656 (1995), Minke & Cook, Physiol. Rev., 82:429-472

(2002)). The structural features include six transmembrane domains, a putative pore region between transmembrane regions 5 and 6, and the absence of charged residues at every third or fourth position in the fourth transmembrane segment. The characteristics of a transmembrane domain are known and include, for instance, several (e.g., ~20) consecutive hydrophobic amino acid residues that allows it to span the thickness of the hydrophobic bilayer. An MscCa polypeptide having structural identity to SEQ ID NO:2 also typically has three ankyrin repeats on the N-terminus (Minke & Cook Physiological Reviews, 82, 429-472 (2002)), and an internal C-terminus in which the 90 terminal amino acids show significant identity to dystrophin, including a coiled-coil structure.